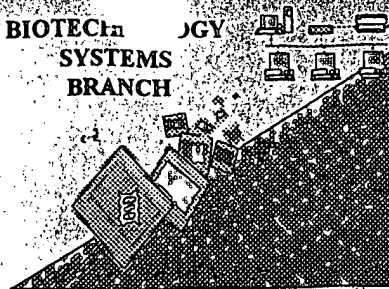


Emphell, B

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/787,328

Source: Per/09

Date Processed by STIC: 6/12/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Please consult Sequence Rules

PCT

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/787,328

DATE: 06/12/2001
TIME: 23:44:55

INPUT SET: S36550.raw

insufficient
mandatory
headings and
responses (see
below)

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

see p 1-2
also, see item 2
on Error Summary

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

(1) General Information:
(ii) Title of invention: NEW HUMAN HEPATOMA-DERIVED GROWTH FACTOR ENCODING SEQUE
AND
POLYPEPTIDE ENCODED BY SUCH DNA SEQUENCE AND PRODUCING METHOD
THEREOF
(iii) Number of Sequences: 8

ERRORED SEQUENCES FOLLOW:

(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1024bp
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

1 ACCGCTCGTC CGCCCGGCTT GAGGCCCGCG GGGAGCGCGC GCAATTCGTC GGCCCGCGGG
61 GGGCGCGCCT CCCGGCATCT TCGCGGCGAC CAAGGACTAC CAGGAAGGGG AGCGGCTGGG
121 ATGGCGCGTC CGCGGCCCCG CGAGTACAAA GCGGGCGACC TGGTCTTCGC CAAGATGAAG
181 GGCTACCCGC ACTGGCCGGC CCGGATTGAT GAACTCCAG AGGGCGCTGT GAAGCCTCCA
241 GCAAACAAGT ATCCTATCTT CTTTTTTGGC ACCCATGAAA CTGCATTTCT AGGTCCCCAA
301 GACCTTTTTC CATATAAGGA GTACAAAGAC AAGTTTGGAA AGTCAAACAA ACGGAAAGGA
361 TTTAACGAAG GATTGTGGGA AATAGAAAAT AACCAGGAG TAAAGTTTAC TGGCTACCAG
421 GCAATTCAGC AACAGAGCTC TTCAGAAACT GAGGGAGAAG GTGGAAATAC TGCAGATGCA
481 AGCAGTGAGG AAGAAGGTGA TAGAGTAGAA GAAGATGGAA AAGGCAAAAG AAAGAATGAA
541 AAAGCAGGCT CAAAACGGAA AAAGTCATAT ACTTCAAAGA AATCCTCTAA ACAGTCCCGG
601 AAATCTCCAG GAGATGAAGA TGACAAAGAC TGCAAAGAAG AGGAAAACAA AAGCAGCTCT
661 GAGGGTGGAG ATGCGGGCAA CGACACAAGA AACACAACCT CAGACTTGCA GAAAACCAAGT
721 GAAGGGACCT AACTACCATA ATGAATGCTG CATATTAAGA GAAACCACAA GAAGGTTATA
781 TGTTTGGTTG TCTAATATTC TTGGATTGTA TATGAACCAA CACATAGTCC TTGTTGTCAT
841 TGACAGAACC CCAGTTTGTA TGTACATTAT TCATATTCCT CTCTGTTGTG TTTCCGGGGG
901 AAAAGACATT TTAGCCTTTT TTAAGAGTTA CTGATTAAAT TTCATGTTAT TTGGTTGCAT
961 GAAGTTGCCC TTAACCACTA AGGATTATCA AGATTTTTCG GCAGACTTAT ACATGTCTAG
102 GATC

SEQUENCE LISTING

(i) GENERAL INFORMATION:
(a) APPLICANT:
(b) TITLE OF INVENTION:
(c) NUMBER OF SEQUENCES:
(d) CORRESPONDENCE ADDRESS:
(1) ADDRESSEE:
(2) STREET:
(3) CITY:
(4) STATE:
(5) COUNTRY:
(6) ZIP:
(e) COMPUTER READABLE FORM:
(1) MEDIUM TYPE:
(2) COMPUTER:
(3) OPERATING SYSTEM:
(4) SOFTWARE:
(f) CURRENT APPLICATION DATA:
(1) APPLICATION NUMBER:
(2) FILING DATE:

insert
these
MANDATORY
headings and
responses for
a U.S. case

invalid - Per Sequence Rules, insert cumulative base total
at right margin of each line

787,328 2

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY linear / linear

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

1 Met Ala Arg Pro Arg Pro Arg Glu Tyr Lys Ala Gly Asp Leu Val
16 Phe Ala Lys Met Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp
31 Glu Leu Pro Glu Gly Ala Val Lys Pro Pro Ala Asn Lys Tyr Pro
46 Ile Phe Phe Phe Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys
61 Asp Leu Phe Pro Tyr Lys Glu Tyr Lys Asp Lys Phe Gly Lys Ser
76 Asn Lys Arg Lys Gly Phe Asn Glu Gly Leu Trp Glu Ile Glu Asn
91 Asn Pro Gly Val Lys Phe Thr Gly Tyr Gln Ala Ile Gln Gln Gln
106 Ser Ser Ser Glu Thr Glu Gly Glu Gly Gly Asn Thr Ala Asp Ala
121 Ser Ser Glu Glu Glu Gly Asp Arg Val Glu Glu Asp Gly Lys Gly
136 Lys Arg Lys Asn Glu Lys Ala Gly Ser Lys Arg Lys Lys Ser Tyr
151 Thr Ser Lys Lys Ser Ser Lys Gln Ser Arg Lys Ser Pro Gly Asp
166 Glu Asp Asp Lys Asp Cys Lys Glu Glu Glu Asn Lys Ser Ser Ser
181 Glu Gly Gly Asp Ala Gly Asn Asp Thr Arg Asn Thr Thr Ser Asp
196 Leu Gln Lys Thr Ser Glu Gly Thr

invalid - Number the amino acids under every 5
amino acids - DO NOT use TAB codes
between amino acid nos. - use space characters

Please replace (globally) MOLECULAR TYPE1 with
MOLECULE TYPE1

FYI: All U.S. applications filed on or
after July 1, 1998, which cannot claim a
prior application filed before July 1, 1998,
must be in new sequence rules
format

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/787,328

DATE: 06/12/2001
TIME: 23:44:55

INPUT SET: S36550.raw

Line	Error	Original Text
32	Entered (1024) and Calc. Seq. Length (0) differ	(A)LENGTH: 1024bp

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/09/787,328*

DATE: 06/12/2001
TIME: 23:44:55

INPUT SET: S36550.raw

APPLICANT
ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
CORRESPONDENCE ADDRESS
MEDIUM TYPE
COMPUTER
OPERATING SYSTEM
SOFTWARE
COMPUTER READABLE FORM
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
CURRENT APPLICATION DATA
APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/187,328

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.